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Sequence Listing could not be accepted.

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Reviewer: Anne Corrigan

Timestamp: Thu Jun 07 15:22:08 EDT 2007

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Reviewer Comments:

<220>

<221> modified_base

<222> (1359)

<223> a, t, c, g, unknown or other

<400> 20

aaaatgattg agaaaggaat cagggagttg atggacccgg aaaatgagat aaggggtaat 1320
gtgaaagtga tgaaaaagga gagtaggana gctgtcgtgg atggtgggac ttcttttgat 1380

The <222> response lists 1359 as the "n" location; however, it is at
location 1349 (see above).

Application No: 10583110

Version No: 1.0

Input Set:**Output Set:****Started:** 2007-06-07 10:32:47.670**Finished:** 2007-06-07 10:32:51.243**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 573 ms**Total Warnings:** 67**Total Errors:** 0**No. of SeqIDs Defined:** 70**Actual SeqID Count:** 70

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
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W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2007-06-07 10:32:47.670
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Total Warnings: 67
Total Errors: 0
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Actual SeqID Count: 70

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> TANAKA, YOSHIKAZU
 ONO, EIICHIRO
 NAKAMURA, NORIKO
 MIZUTANI, MASAKO

<120> METHOD FOR PRODUCING YELLOW FLOWER BY CONTROLLING
 FLAVONOID SYNTHETIC PATHWAY

<130> 47237.5008/00US

<140> 10583110

<141> 2007-06-07

<150> 10/583,110

<151> 2006-06-15

<150> PCT/JP2004/019461

<151> 2004-12-17

<150> JP 2003-420046

<151> 2003-12-17

<160> 70

<170> PatentIn Ver. 3.3

<210> 1

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1371)

<220>

<223> Description of Artificial Sequence: Synthetic
 nucleotide construct

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Met Gly Glu Glu Tyr Lys Lys Thr His Thr Ile Val Phe His Thr Ser	
1 5 10 15	

gaa gaa cac ctc aac tct tca ata gcc ctt gca aag ttc ata acc aaa	96
Glu Glu His Leu Asn Ser Ser Ile Ala Leu Ala Lys Phe Ile Thr Lys	
20 25 30	

cac cac tct tca atc tcc atc act atc atc agc act gcc ccc gcc gaa	144
His His Ser Ser Ile Ser Ile Thr Ile Ile Ser Thr Ala Pro Ala Glu	
35 40 45	

tct tct gaa gtg gcc aaa att att aat aat ccg tca ata act tac cgc	192
Ser Ser Glu Val Ala Lys Ile Ile Asn Asn Pro Ser Ile Thr Tyr Arg	
50 55 60	

ggc ctc acc gcg gta gcg ctc cct gaa aat ctc acc agt aac att aat	240
Gly Leu Thr Ala Val Ala Leu Pro Glu Asn Leu Thr Ser Asn Ile Asn	
65 70 75 80	
aaa aac ccc gtc gaa ctt ttc ttc gaa atc cct cgt cta caa aac gcc	288
Lys Asn Pro Val Glu Leu Phe Phe Glu Ile Pro Arg Leu Gln Asn Ala	
85 90 95	
aac ctt cga gag gct tta cta gat att tcg cga aaa tcc gat atc aaa	336
Asn Leu Arg Glu Ala Leu Leu Asp Ile Ser Arg Lys Ser Asp Ile Lys	
100 105 110	
gca tta atc atc gat ttc ttc tgc aat gcg gca ttt gaa gta tcc acc	384
Ala Leu Ile Ile Asp Phe Phe Cys Asn Ala Ala Phe Glu Val Ser Thr	
115 120 125	
agc atg aac ata ccc act tac ttc gac gtc agt ggc ggc gct ttt ctc	432
Ser Met Asn Ile Pro Thr Tyr Phe Asp Val Ser Gly Gly Ala Phe Leu	
130 135 140	
ctc tgc acg ttt ctc cac cac ccg aca cta cac caa act gtt cgt gga	480
Leu Cys Thr Phe Leu His His Pro Thr Leu His Gln Thr Val Arg Gly	
145 150 155 160	
gac att gcg gat ttg aac gat tct gtt gag atg ccc ggg ttc cca ttg	528
Asp Ile Ala Asp Leu Asn Asp Ser Val Glu Met Pro Gly Phe Pro Leu	
165 170 175	
att cac tcc tct gat tta cca atg agt ttg ttt tat cgt aag act aat	576
Ile His Ser Ser Asp Leu Pro Met Ser Leu Phe Tyr Arg Lys Thr Asn	
180 185 190	
gtt tac aaa cac ttt cta gac act tcc tta aac atg cgc aaa tcg agt	624
Val Tyr Lys His Phe Leu Asp Thr Ser Leu Asn Met Arg Lys Ser Ser	
195 200 205	
ggg ata ctc gtg aac acg ttt gtt gcg ctc gag ttt cga gct aag gaa	672
Gly Ile Leu Val Asn Thr Phe Val Ala Leu Glu Phe Arg Ala Lys Glu	
210 215 220	
gct ttg tcc aac ggt ttg tac ggt cca act ccg cct ctt tat tta ctt	720
Ala Leu Ser Asn Gly Leu Tyr Gly Pro Thr Pro Pro Leu Tyr Leu Leu	
225 230 235 240	
tca cat aca att gcc gaa ccc cac gac act aaa gtg ttg gta aac caa	768
Ser His Thr Ile Ala Glu Pro His Asp Thr Lys Val Leu Val Asn Gln	
245 250 255	
cac gaa tgc cta tca tgg ctt gat ttg cag cct agt aaa agc gtg att	816
His Glu Cys Leu Ser Trp Leu Asp Leu Gln Pro Ser Lys Ser Val Ile	
260 265 270	
ttc ctt tgt ttc gga aga aga gga gcg ttc tca gca caa cag ttg aaa	864
Phe Leu Cys Phe Gly Arg Arg Gly Ala Phe Ser Ala Gln Gln Leu Lys	
275 280 285	

gaa att gcg ata ggg ttg gag aag agt gga tgt cga ttt ctt tgg ttg	912
Glu Ile Ala Ile Gly Leu Glu Lys Ser Gly Cys Arg Phe Leu Trp Leu	
290 295 300	
gcc cgc att tca ccg gag atg gac tta aat gcg ctt ctg ccg gag ggt	960
Ala Arg Ile Ser Pro Glu Met Asp Leu Asn Ala Leu Leu Pro Glu Gly	
305 310 315 320	
ttt cta tcg aga act aaa gga gta ggg ttt gtg aca aac aca tgg gtg	1008
Phe Leu Ser Arg Thr Lys Gly Val Gly Phe Val Thr Asn Thr Trp Val	
325 330 335	
ccg caa aaa gag gtg ttg agt cat gat gca gtg ggg ggg ttt gtg act	1056
Pro Gln Lys Glu Val Leu Ser His Asp Ala Val Gly Gly Phe Val Thr	
340 345 350	
cat tgc ggg tgg agt tcg gtt ctt gaa gcg ctg tcg ttc ggt gtc ccg	1104
His Cys Gly Trp Ser Ser Val Leu Glu Ala Leu Ser Phe Gly Val Pro	
355 360 365	
atg att ggt tgg ccg ttg tac gca gag cag agg atc aat agg gtg ttc	1152
Met Ile Gly Trp Pro Leu Tyr Ala Glu Gln Arg Ile Asn Arg Val Phe	
370 375 380	
atg gtg gag gaa ata aag gtg gcg ctg cca ttg gat gag gaa gat gga	1200
Met Val Glu Glu Ile Lys Val Ala Leu Pro Leu Asp Glu Glu Asp Gly	
385 390 395 400	
ttt gtg acg gcg atg gag ttg gag aag cgc gtc agg gag ttg atg gag	1248
Phe Val Thr Ala Met Glu Leu Glu Lys Arg Val Arg Glu Leu Met Glu	
405 410 415	
tcg gta aag ggg aaa gaa gtg aag cgc cgt gtg gcg gaa ttg aaa atc	1296
Ser Val Lys Gly Lys Glu Val Lys Arg Arg Val Ala Glu Leu Lys Ile	
420 425 430	
tct aca aag gca gcc gtg agt aaa ggt gga tcg tcc ttg gct tct ttg	1344
Ser Thr Lys Ala Ala Val Ser Lys Gly Gly Ser Ser Leu Ala Ser Leu	
435 440 445	
gag aag ttc atc aac tcg gtc act cgt taaagtttct tactcaatat	1391
Glu Lys Phe Ile Asn Ser Val Thr Arg	
450 455	
atggtacatc gggttaacta ccaaatttta t	1422

<210> 2

<211> 457

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein

<400> 2

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Glu	Glu	His	Leu	Asn	Ser	Ser	Ile	Ala	Leu	Ala	Lys	Phe	Ile	Thr	Lys	20	25	30	
His	His	Ser	Ser	Ile	Ser	Ile	Thr	Ile	Ile	Ser	Thr	Ala	Pro	Ala	Glu	35	40	45	
Ser	Ser	Glu	Val	Ala	Lys	Ile	Ile	Asn	Asn	Pro	Ser	Ile	Thr	Tyr	Arg	50	55	60	
Gly	Leu	Thr	Ala	Val	Ala	Leu	Pro	Glu	Asn	Leu	Thr	Ser	Asn	Ile	Asn	65	70	75	80
Lys	Asn	Pro	Val	Glu	Leu	Phe	Phe	Glu	Ile	Pro	Arg	Leu	Gln	Asn	Ala	85	90	95	
Asn	Leu	Arg	Glu	Ala	Leu	Leu	Asp	Ile	Ser	Arg	Lys	Ser	Asp	Ile	Lys	100	105	110	
Ala	Leu	Ile	Ile	Asp	Phe	Phe	Cys	Asn	Ala	Ala	Phe	Glu	Val	Ser	Thr	115	120	125	
Ser	Met	Asn	Ile	Pro	Thr	Tyr	Phe	Asp	Val	Ser	Gly	Gly	Ala	Phe	Leu	130	135	140	
Leu	Cys	Thr	Phe	Leu	His	His	Pro	Thr	Leu	His	Gln	Thr	Val	Arg	Gly	145	150	155	160
Asp	Ile	Ala	Asp	Leu	Asn	Asp	Ser	Val	Glu	Met	Pro	Gly	Phe	Pro	Leu	165	170	175	
Ile	His	Ser	Ser	Asp	Leu	Pro	Met	Ser	Leu	Phe	Tyr	Arg	Lys	Thr	Asn	180	185	190	
Val	Tyr	Lys	His	Phe	Leu	Asp	Thr	Ser	Leu	Asn	Met	Arg	Lys	Ser	Ser	195	200	205	
Gly	Ile	Leu	Val	Asn	Thr	Phe	Val	Ala	Leu	Glu	Phe	Arg	Ala	Lys	Glu	210	215	220	
Ala	Leu	Ser	Asn	Gly	Leu	Tyr	Gly	Pro	Thr	Pro	Pro	Leu	Tyr	Leu	Leu	225	230	235	240
Ser	His	Thr	Ile	Ala	Glu	Pro	His	Asp	Thr	Lys	Val	Leu	Val	Asn	Gln	245	250	255	
His	Glu	Cys	Leu	Ser	Trp	Leu	Asp	Leu	Gln	Pro	Ser	Lys	Ser	Val	Ile	260	265	270	
Phe	Leu	Cys	Phe	Gly	Arg	Arg	Gly	Ala	Phe	Ser	Ala	Gln	Gln	Leu	Lys	275	280	285	
Glu	Ile	Ala	Ile	Gly	Leu	Glu	Lys	Ser	Gly	Cys	Arg	Phe	Leu	Trp	Leu	290	295	300	

Ala Arg Ile Ser Pro Glu Met Asp Leu Asn Ala Leu Leu Pro Glu Gly
305 310 315 320

Phe Leu Ser Arg Thr Lys Gly Val Gly Phe Val Thr Asn Thr Trp Val
325 330 335

Pro Gln Lys Glu Val Leu Ser His Asp Ala Val Gly Gly Phe Val Thr
340 345 350

His Cys Gly Trp Ser Ser Val Leu Glu Ala Leu Ser Phe Gly Val Pro
355 360 365

Met Ile Gly Trp Pro Leu Tyr Ala Glu Gln Arg Ile Asn Arg Val Phe
370 375 380

Met Val Glu Glu Ile Lys Val Ala Leu Pro Leu Asp Glu Glu Asp Gly
385 390 395 400

Phe Val Thr Ala Met Glu Leu Glu Lys Arg Val Arg Glu Leu Met Glu
405 410 415

Ser Val Lys Gly Lys Glu Val Lys Arg Arg Val Ala Glu Leu Lys Ile
420 425 430

Ser Thr Lys Ala Ala Val Ser Lys Gly Gly Ser Ser Leu Ala Ser Leu
435 440 445

Glu Lys Phe Ile Asn Ser Val Thr Arg
450 455

<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 3
gaaatggtcg gattggctgg g 21

<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 4
acctccaccc caactttcag g 21

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 5
gatgcataat ttggctagaa aagc 24

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 6
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<210> 7
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 7
tgccctcgaat gggttgagcac g 21

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 8
ctctcactct cacaccg 18

<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 9
cacgaatgct tagcatggct c 21

<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 10
cttattgccc actgaaaccc c 21

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 11
tgtctgaatt ggcttgattc c 21

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 12
aaccacaga aaccctgtt c 21

<210> 13
<211> 1446
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic nucleotide construct

<400> 13

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gccttcgctg atccgataaa caaagctcgt gattcggggc tcgatattgg actaagcatc 180
ctcaaattcc caccagaagg atcaggaata ccagatcaca tggtagacct tgatctagtt 240
actgaagatt ggctcccaaa gtttgttgag tcattagtct tattacaaga gccagttgag 300
aagcttatcg aagaactaaa gctcgactgt ctcgtttccg acatgttctt gccttggaaca 360
gtcgattgtg cggctaagtt cggatttccg aggttggttt tccacggaac gagcaacttt 420
gcgttgtgtg cttcggagca aatgaagctt cacaagcctt ataagaatgt aacttctgat 480
actgagacat ttgttatacc ggattttccg catgagctga agtttgtgag gactcaagtg 540
gctccgtttc agcttgcgga aacggagaat ggattctcaa agttgatgaa acagatgacg 600
gagtctgttg gtagaagcta cgggtgtgtg gttaacagtt tttatgagct cgagtcgact 660
tatgtggatt attacagaga ggttttggtt agaaagtctt ggaatatagg gcctctgttg 720
ttatccaaca atggcaatga ggaaaaagta caaaggggaa aggaatctgc gattggcgaa 780
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ggaagtatgg cgactttttac tccagcgagc ttgctcgaaa ctgagattgg actcgaggaa 900
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cattgtggat ggaattcgac gttggaagga atatgcgcg gtgtgcctat ggtgacttgg 1140
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gcgaagtatt ataaggaaat ggcgaggcgg gcggttgagg aaggcggttc gtcttataat 1380
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aactag 1446
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<210> 14

<211> 1488

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 14

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acgatcatcg taacacctct taacgcgcga cgattcaatt ccgttattaa tcgagccggt 180
gaatcaggac agtccattcg tcttctccaa gtaaaattcc ctggtgaaga agccgggttg 240
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cgaattccga ggataatttt cgatggaatg agctgttttg ctcctttagt aacacacggt 480
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gttaaaaccg aaggagagaa gtcgttggaa atagagaaat ggattttgga caatggattc 1020
gaggaaagaa cgaaagatag agggttcttg attcgtggtt ggtcgccaca agtggtgatc 1080
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gagaagttag tgggtgcagat tttggggacg ggtgtgggag ttggagcgaa aagtacggta 1260
catttggggg atgaagagat ggatgagatg agagtgacga ggaaggggat taccaaggcg 1320
gtcgtggcag ttatggatag aggaactgaa ggtgttgaga ggcggagaaa ggcgaaggag 1380
cttggtgaaa tggctaagag ggcagtccaa gttgggggat cttcatgtaa gaatgtcgac 1440
cagctaattc aagaagttgc accattgagt gtagcgaggg atgtgtaa 1488

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<210> 15

<211> 1446

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 15

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cacataacct tcgtcaacac cgagtacatc cgtctccgcc tcctcaagtc ctgtggccct 180
gccgccctgg acgggctacc ggactttcgc ttcatgacta tccccgatgg cctccctttg 240
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catcttgtgg agagaggata tgtacctctc aaagatacga gccca

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